

# BEST AVAILABLE COPY

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Commissioner for Patents  
P.O. Box 1450  
Alexandria, VA 22313-1450

On April 28, 2005

TOWNSEND and TOWNSEND and CREW LLP

By: Patricia Anders

PATENT

Attorney Docket No.: 02307E-114910US  
Client Ref. No.: 2001-124-2

## IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:

Zuker et al.

Application No.: 10/026,188

Filed: December 21, 2001

For: ASSAYS FOR TASTE RECEPTOR  
CELL SPECIFIC ION CHANNEL

Customer No.: 20350

Confirmation No. 9521

Examiner: Michael T. Brannock

Technology Center/Art Unit: 1646

Declaration of Charles S. Zuker and Yifeng

Zhang pursuant to 37 C. F. R. §1.131

Commissioner for Patents  
P.O. Box 1450  
Alexandria, VA 22313-1450

Sir:

We, Charles S. Zuker and Yifeng Zhang, being duly warned that willful false statements and the like are punishable by fine or imprisonment or both, under 18 U.S.C. §1001, and may jeopardize the validity of the patent application or any patent issuing thereon, state and declare as follows:

1. All statements herein made of our own knowledge are true and statements made on information or belief are believed to be true. Exhibits I-V are attached hereto and incorporated herein by reference.

2. At the time this invention was first conceived, we were employees of Howard Hughes Medical Institute and the University of California, located in San Diego, California. All activities described in this Declaration took place in the United States of America.

3. In accordance with 37 C.F.R. §1.131, we state that we completed the claimed invention in the United States prior to April 17, 2000, the filing date of USSN 60/197,491, to which published U.S. Patent Application US 2002/0037515 claims priority.

4. Attached to this Declaration are:

Exhibit I, pages of a printout of a sequence file containing the polynucleotide sequence of 930 clones obtained from a subtracted cDNA library prepared from rat circumvallate cells, following the experimental procedure described in Example I of the application. The pages of Exhibit I indicate the date of last modification to contiguous sequence ("contig") No. 068-3 157 501 and the polynucleotide sequence of clone 501, one of the three clones that make up this contig;

Exhibit II, pages of laboratory notebook indicating that a Blast search was performed for known polynucleotide sequences matching each one of the 930 clones, including clone 501;

Exhibit III, results of sequence alignment between the mouse Trpm5 (also known as Mtr1 and Ltrpc5) and clone 501, which indicate a high degree of homology;

Exhibit IV, polynucleotide sequences of the mouse Trpm5 (GenBank No. NM\_020277, derived from GenBank No. AJ271092, see page 2 of printout for NM\_020277) and human Mtr1 (GenBank No. AF177473), which indicate that these sequences were publicly accessible by January 14, 2000 (see page 1 of printout for AJ271092) and August 13, 1999 (see page 1 of printout for AF177473), respectively. Exhibit IV further includes results of a sequence alignment between the amino acid sequences encoded by mouse Trpm5 gene and human Mtr1 gene; and

Exhibit V, results of an *in situ* hybridization experiment indicating the taste cell-specific expression of the gene from which clone 501 is derived, using a nucleic acid probe specific for clone 501, which was also referred to as 501-PCR46. Some dates in the Exhibits have been redacted. All redacted dates in the Exhibits are prior to April 17, 2000.

5. Conception of the present invention as well as its reduction to practice are evidenced by Exhibits I-IV. The first page of Exhibit I shows that contig No. 068-3 157 501 consists of three clones: 3, 157, and 501, the longest of which is clone 501. The second page shows the polynucleotide sequence of clone 501. The third page establishes the time of last modification made to contig No. 068-3 157 501 and therefore establishes the time when the sequence of clone 501 was determined. Upon determination of the polynucleotide sequence of clone 501, a Blast search was conducted to identify known polynucleotide sequence(s) with high level of sequence homology with clone 501. This is evidenced by Exhibit II.

6. The identification of the mouse Trpm5 gene through this sequence homology-based search is evidenced by Exhibit III, which demonstrates that the mouse Trpm5 and clone 501 are highly homologous. Therefore, one of skill in the art would consider the rat gene from which clone 501 is derived to be the ortholog of mouse Trpm5. Although this particular sequence alignment shown in Exhibit III was performed at the present time, the same result would have been (and was indeed) obtained at the time the initial Blast search was performed. This is because, as evidenced by Exhibit IV, the polynucleotide sequence of mouse Trpm5 was publicly accessible well before April 17, 2000. Furthermore, Exhibit IV establishes that human Mtr1 and mouse Trpm5 have a greater than 84% identity in amino acid sequence. Based on this high level of sequence homology, one of skill in the art would recognize human Mtr1 as the ortholog of mouse Trpm5. In addition, Exhibit IV also demonstrates that the polynucleotide sequence of human Mtr1 gene was publicly available well before April 17, 2000. Thus, a Blast search based on the sequence of clone 501 by the present inventors at the time indicated by Exhibit II necessarily led to the identification of both the human and mouse versions of the Mtr1 gene. Subsequently, *in situ* hybridization was performed to confirm the taste cell-specific expression of the rat version of this gene, shown in Exhibit V. It is therefore established that,

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Declaration under 37 C.F.R. §1.131  
Reply to Office Action of November 30, 2004

PATENT

prior to April 17, 2000, the present inventors had identified the human, mouse, and rat Mtr1 genes as taste cell specific ion channels.

7. In light of the foregoing, it is established that Declarants had in their possession the claimed subject matter of the present invention prior to the effective filing date of the published U.S. Patent Application US 2002/0037515.

8. Declarants have nothing further to say.

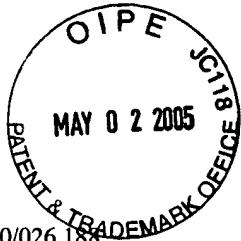
Dated: 4/13/05

By:   
Charles S. Zuker, Ph.D.

Dated: \_\_\_\_\_

By: \_\_\_\_\_  
Yifeng Zhang, Ph.D.

Attachments (Exhibits I-V)  
60427031 V1



Appl. No. 10/026,188

PATENT

Declaration under 37 C.F.R. §1.131

Reply to Office Action of November 30, 2004

prior to April 17, 2000, the present inventors had identified the human, mouse, and rat Mtr1 genes as taste cell specific ion channels.

7. In light of the foregoing, it is established that Declarants had in their possession the claimed subject matter of the present invention prior to the effective filing date of the published U.S. Patent Application US 2002/0037515.

8. Declarants have nothing further to say.

Dated: \_\_\_\_\_

By: \_\_\_\_\_  
Charles S. Zuker, Ph.D.

Dated: 4/20/05

By: \_\_\_\_\_  
Yifeng Zhang, Ph.D.

Attachments (Exhibits I-V)  
60427031 V1

Rat Sub Seq 12/99 copy  
Sequencher™ "Rat Sub Seq 12/99 copy"

Name	Size	Kind	Label	Last Modified
042 GS	205 BPs	AutoSeq Frag, ABI	-	Thu, Jan 27, 2000 2:58:
043 GS	392 BPs	AutoSeq Frag, ABI	-	Thu, Jan 27, 2000 2:59:
044 86	700 BPs	Contig of 2	-	Fri, Jan 14, 2000 6:44:
045	284 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:33:
046 GS	486 BPs	AutoSeq Frag, ABI	-	Thu, Jan 27, 2000 2:59:
047	192 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:24:
048 GS	256 BPs	AutoSeq Frag, ABI	-	Thu, Jan 27, 2000 3:00:
049 262-5 GS	408 BPs	Contig of 2	-	Thu, Jan 27, 2000 3:07:
050 120 659	571 BPs	Contig of 3	-	Thu, Feb 3, 2000 8:14:
051 854	350 BPs	Contig of 2	-	Thu, Feb 3, 2000 8:14:
052	603 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:24:
053 3'	105 BPs	DNA Fragment	-	Fri, Jan 14, 2000 6:32:
053-5 487-5 GS	309 BPs	Contig of 2	-	Thu, Jan 27, 2000 3:49:
053mid 303	268 BPs	Contig of 2	-	Wed, Jan 19, 2000 6:19:
054	502 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:32:
054 5' ok	102 BPs	DNA Fragment	-	Thu, Jan 27, 2000 3:09:
055 3' ok	156 BPs	DNA Fragment	-	Thu, Jan 27, 2000 3:09:
055 5'	544 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:31:
056	87 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:24:
057 76 178.464 515-...	252 BPs	Contig of 7	-	Thu, Feb 3, 2000 11:1:
059	330 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:24:
060 895-3 ok	307 BPs	Contig of 2	-	Thu, Jan 27, 2000 3:11:
061	43 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:24:
062	453 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:24:
063 GS	222 BPs	AutoSeq Frag, ABI	-	Thu, Jan 27, 2000 3:13:
064	609 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:24:
065 3'	85 BPs	DNA Fragment	-	Fri, Jan 14, 2000 6:31:
066 5' ok	541 BPs	AutoSeq Frag, ABI	-	Thu, Jan 27, 2000 3:16:
067	580 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:24:
068 5' ok	117 BPs	DNA Fragment	-	Thu, Jan 27, 2000 3:17:
068 3 157 501	629 BPs	Contig of 3	-	
069 GS	209 BPs	AutoSeq Frag, ABI	-	Thu, Jan 27, 2000 3:19:
070 493-5 648-5	351 BPs	Contig of 3	-	Thu, Feb 3, 2000 11:1:
071	560 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:24:
072 3'	104 BPs	DNA Fragment	-	Fri, Jan 14, 2000 6:30:
072 5'	578 BPs	AutoSeq Frag, ABI	-	Fri, Jan 14, 2000 6:30:
073 815-3	544 BPs	Contig of 2	-	Fri, Jan 14, 2000 6:49:
074 GS	439 BPs	AutoSeq Frag, ABI	-	Thu, Jan 27, 2000 3:20:
075 510 229 831 88...	322 BPs	Contig of 6	-	Wed, Jan 19, 2000 6:19:
078 GS	587 BPs	AutoSeq Frag, ABI	-	Thu, Jan 27, 2000 3:22:

# Differential Screening + Sequencing

Colony lifts w/ blue-white selection

Hybrid N+ lifts  
autoclave 5'  
rinse to get rid of the debris

Hyb: w/ sub- (reverse subtracted) as probe.

Pick white colonies (930)

Miniprep (Clontech 96)

Sequencing (5 μl of each DNA sample)

Report

930 Seg. ran

74 bad seg

856 good or seg

57 have  
≥ 2 pieces of inserts

799 have only one inserts

total 933 DNA fragments (w/ seg.)

104 contigs

80 pairs

16 triplets

2 contig of 4

1 contig of 5

2 contig of 6

1 contig of 7

2 contig of 9

655 unique DNA fragments

325 unknown by some hits

61 no hits

14 w/ >1 Tm (none of them g)

8 full length homologs w/ unknown functions, but no Tm at all

9 full length homologs, unknown functions  
≥ 1 Tm

others known genes

(Continued)

II. SF-G15 ~~Final Assay~~

Not Working !!

Cell lines tried

① Peak Rapid Rb Gx15

② Peak Rapid





## Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

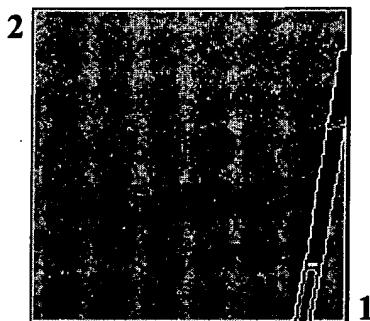
Structure

### BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.10 [Oct-19-2004]

Match:  Mismatch:  gap open:  gap extension:   
 x\_dropoff:  expect:  wordsize:  Filter

**Sequence 1** gi 12383053 Mus musculus transient receptor potential cation channel, subfamily M, member 5 (Trpm5), mRNA **Length 4032 (1 .. 4032)**

**Sequence 2** lcl|501 contig **Length 627 (1 .. 627)**



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 371 bits (193), Expect = 7e-99  
 Identities = 349/414 (84%), Gaps = 9/414 (2%)  
 Strand = Plus / Plus

Query: 3583 ccttgctacagatcacttcttggacatcccttcctaagagaatgaaaactcatgtcttgg 3642  
 Sbjct: 127 ccttgccgcagaccatgtcttggacaccttccttatgaaaatgagactcatgtcttgg 186

Query: 3643 catctattcgggagcctcagaagtatcctccaggcaggcaagatttcatgtccac 3702  
 Sbjct: 187 catctatctggagccccaggcgt--cctctccaggcaggcaagtttcatgtccac 244

Query: 3703 -taaagctttcactggcttggactggacagctggatctggccaagtccatacataggacac 3761  
 Sbjct: 248 -taaagctttcactggcttggactggacagctggatctggccaagtccatacataggacac 244

· Sbjct: 245 ctaaaaactttcaccagctaagactggacagctggaaactggccaagtcccacatgggatac 304

Query: 3762 catctgcctggatgggctatttaggtctaaccctgtcttaccctgagttcctaagaag 3821

||||||||||||||||||| ||| ||||| ||| ||||||||||||||| ||||| |

Sbjct: 305 catctgcctggatgggctacttacgtctagcc--tgtcttaccctgagttccaaagagg 362

Query: 3822 ccaacctttaaacactag--gtttcttct-gaccctgaccactcattagctgacca 3878

||||||||||||||||||| ||| ||||| ||| ||||||| ||| ||||| ||||| |

Sbjct: 363 ccaacctttaaacactagactagaggttccttctgtatccatccatcagccgacca 422

Query: 3879 gctcctagagggcaggactcagatctattgttaattacccatcttcaccccccacag 3938

||| ||||||||||||||||| ||| ||||| | ||||||| ||| ||||| ||||| |

Sbjct: 423 gcttctagagggcaggactcagatctactgttaatcagctccatcctcagcccccacag 482

Query: 3939 cattatctgtctgatcattctggca-gaaaccccaagatattgctcaagggtac 3991

||| ||| ||| ||||| | ||||||| ||||||||||||| ||| ||||||| |

Sbjct: 483 cataatttgtgtatygcttgcacaaaaccccaagatactgytcaagggtac 536

Score = 160 bits (83), Expect = 3e-35

Identities = 114/127 (89%), Gaps = 1/127 (0%)

Strand = Plus / Plus



Query: 3442 acctagagtctggcttgcaccctctgacacctgaaatggagaaaccacttgctctagag 3501

||||||| ||||||||||||| ||| ||||||| ||||||||||||| ||| ||||||| |

Sbjct: 1 acctagaggctggcttgcacactcagacacctgaaatggagaaaccacttgccttagag 60

Query: 3502 ccccagacctggccacatcgagtttgggcacatcaaccccccactccagcagc 3561

||| ||||||||||||| ||| ||||| ||||||||||||| ||| ||||||| |

Sbjct: 61 ctccagacctggccagattgagtttggtcacatcaacccctgc-cccagcagc 119

Query: 3562 cccaaaga 3568

||| |||

Sbjct: 120 cccgaga 126

CPU time: 0.02 user secs. 0.01 sys. secs 0.03 total secs.

Lambda K H  
1.33 0.621 1.12

Gapped

Lambda K H  
1.33 0.621 1.12

Matrix: blastn matrix:1 -2

Gap Penalties: Existence: 5, Extension: 2

Number of Sequences: 1  
Number of Hits to DB: 69  
Number of extensions: 11  
Number of successful extensions: 8  
Number of sequences better than 10.0: 1  
Number of HSP's better than 10.0 without gapping: 1  
Number of HSP's gapped: 2  
Number of HSP's successfully gapped: 2  
Number of extra gapped extensions for HSPs above 10.0: 0  
Length of query: 4032  
Length of database: 13,373,181,452  
Length adjustment: 27  
Effective length of query: 4005  
Effective length of database: 13,373,181,425  
Effective search space: 53559591607125  
Effective search space used: 53559591607125  
Neighboring words threshold: 0  
Window for multiple hits: 0  
X1: 11 (21.1 bits)  
X2: 26 (50.0 bits)  
X3: 26 (50.0 bits)  
S1: 12 (23.8 bits)  
S2: 22 (43.0 bits)


[PubMed](#) [Nucleotide](#) [Protein](#) [Genome](#) [Structure](#) [PMC](#) [Taxonomy](#) [OMIM](#) [Books](#)
**Search** **Nucleotide** **for** **Go** **Clear**
[Limits](#) [Preview/Index](#) [History](#) [Clipboard](#) [Details](#)
**Display****GenBank****Send****all to file**

Range: from  to   Reverse complemented strand Features:  SNP  CDD  
 MGC  HPRD

1: NM\_020277. Reports *Mus musculus* tran...[gi:12383053]

Links

**LOCUS** NM\_020277 4032 bp mRNA linear ROD 26-OCT-2004  
**DEFINITION** *Mus musculus* transient receptor potential cation channel, subfamily M, member 5 (Trpm5), mRNA.  
**ACCESSION** NM\_020277  
**VERSION** NM\_020277.1 GI:12383053  
**KEYWORDS**  
**SOURCE** *Mus musculus* (house mouse)  
**ORGANISM** *Mus musculus*  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
**REFERENCE** 1 (bases 1 to 4032)  
**AUTHORS** Liu,D. and Liman,E.R.  
**TITLE** Intracellular Ca<sup>2+</sup> and the phospholipid PIP2 regulate the taste transduction ion channel TRPM5  
**JOURNAL** Proc. Natl. Acad. Sci. U.S.A. 100 (25), 15160-15165 (2003)  
**PUBMED** 14657398  
**REMARK** GeneRIF: regulation of TRPM5 by Ca<sup>2+</sup> mediates sensory activation in the taste system  
**REFERENCE** 2 (bases 1 to 4032)  
**AUTHORS** Hofmann,T., Chubanov,V., Gudermann,T. and Montell,C.  
**TITLE** TRPM5 is a voltage-modulated and Ca(2+)-activated monovalent selective cation channel  
**JOURNAL** Curr. Biol. 13 (13), 1153-1158 (2003)  
**PUBMED** 12842017  
**REFERENCE** 3 (bases 1 to 4032)  
**AUTHORS** Perez,C.A., Huang,L., Rong,M., Kozak,J.A., Preuss,A.K., Zhang,H., Max,M. and Margolskee,R.F.  
**TITLE** A transient receptor potential channel expressed in taste receptor cells  
**JOURNAL** Nat. Neurosci. 5 (11), 1169-1176 (2002)  
**PUBMED** 12368808  
**REMARK** GeneRIF: functions as a cationic channel that is gated when internal calcium stores are depleted and may be responsible for capacitative calcium entry in taste receptor cells that respond to bitter and/or sweet compounds.  
**REFERENCE** 4 (bases 1 to 4032)  
**AUTHORS** Paulsen,M., El-Maarri,O., Engemann,S., Strodticke,M., Franck,O., Davies,K., Reinhardt,R., Reik,W. and Walter,J.  
**TITLE** Sequence conservation and variability of imprinting in the Beckwith-Wiedemann syndrome gene cluster in human and mouse  
**JOURNAL** Hum. Mol. Genet. 9 (12), 1829-1841 (2000)  
**PUBMED** 10915772  
**REFERENCE** 5 (bases 1 to 4032)  
**AUTHORS** Enklaar,T., Esswein,M., Oswald,M., Hilbert,K., Winterpacht,A., Higgins,M., Zabel,B. and Prawitt,D.  
**TITLE** Mtr1, a novel biallelically expressed gene in the center of the mouse distal chromosome 7 imprinting cluster, is a member of the Trp gene family

JOURNAL Genomics 67 (2), 179-187 (2000)  
 PUBMED [10903843](#)  
 REFERENCE 6 (bases 1 to 4032)  
 AUTHORS Yatsuki, H., Watanabe, H., Hattori, M., Joh, K., Soejima, H., Komoda, H., Xin, Z., Zhu, X., Higashimoto, K., Nishimura, M., Kuratomi, S., Sasaki, H., Sakaki, Y. and Mukai, T.  
 TITLE Sequence-based structural features between Kvlqt1 and Tapal on mouse chromosome 7F4/F5 corresponding to the Beckwith-Wiedemann syndrome region on human 11p15.5: long-stretches of unusually well conserved intronic sequences of kvlqt1 between mouse and human  
 JOURNAL DNA Res. 7 (3), 195-206 (2000)  
 PUBMED [10907850](#)  
 COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final NCBI review. The reference sequence was derived from [AJ271092.2](#).  
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   /note="synonyms: Mtr1, Ltrpc5, 9430099A16Rik"  
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   /db\_xref="MGI:1861718"  
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   /function="TRP channel"  
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   go\_function: ion channel activity [goid [0005216](#)] [evidence IEA];  
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   go\_process: ion transport [goid [0006811](#)] [evidence IEA]"  
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   PIHYPADEGNIQGPLCPLDSNLSHFILEVESGALGSGNDGLTELQLSLEKHISQQRTGY  
   GGTSCIQIPVLCLLVNGDPNTLERISRAVEQAAPWLILAGSGGIADVLAALVSQPHLL  
   VPQVAEKQFREKFPSECFSWEAIVHWTLLQNIAAHPHLLTVYDFEQEGSEDLDTVIL  
   KALVKACKSHSQEAQDYLDELKLAVALDRVDIAKSEIFNGDVEWKSCDLEEVMTDALV  
   SNKPDFVRLFVDSGADMAEFLTYGRLQQLYHSVSPKSLLFELLQRKHEEGRRTLGLG  
   AQQARELPIGLPAFSLHEVSRVLKDFLHDACRGFYQDGRRMEERGPPKRPAGQKWLKD  
   LSRKSEDPWRDLFLWAVLQNRYEMATYFWAMREGVAAALAACKIIKEMSHLEKEAEV  
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LIAMFSYTFQVVQGNADMFWKFQRYHLIVEYHGRPALAPPFILLSHLSVLKQVFRKE  
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 ST"

## ORIGIN

1 atgcaaacaa cccagagctc ctgccccggc agccccccag atactgagga tggctggag  
 61 cccatcttat gcaggggaga gatcaacttc ggagggtctg ggaagaagcg aggcaagttt  
 121 gtgaaggtgc caagcagtgt ggccccctcc gtgttttg aactcctgct caccgagtgg  
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NCBI Nucleotide

PubMed Nucleotide Protein Genome Structure PMC Taxonomy OMIM Books

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Display GenBank

Range: from  to   Reverse complemented strand Features:  SNP  CDD  
 MGC  HPRD

1: [AJ271092](#). Reports ...[gi:8546859] The record has been replaced by [AJ271092.2](#)

**LOCUS** MMU271092 4691 bp mRNA linear ROD 03-AUG-2000

**DEFINITION** *Mus musculus* partial mRNA for *Ltrcp5* protein (*Ltrpc5* gene).

**ACCESSION** AJ271092

**VERSION** AJ271092.1 GI:8546859

**KEYWORDS** *Ltrpc5* gene; *Ltrpc5* protein.

**SOURCE** *Mus musculus* (house mouse)

**ORGANISM** *Mus musculus*  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; *Mus*.

**REFERENCE** 1 (bases 1 to 4691)

**AUTHORS** Paulsen,M., El-Maarrri,O., Engemann,S., Stroedel,M., Franck,O., Davies,K., Reinhardt,R., Reik,W. and Walter,J.

**TITLE** Sequence conservation and variability of imprinting in the Beckwith-Wiedemann syndrome gene cluster in human and mouse

**JOURNAL** *Hum. Mol. Genet.* 9 (12), 1829-1841 (2000)

**MEDLINE** [20377495](#)

**REFERENCE** 2 (bases 1 to 4691)

**AUTHORS** Stroedel,M.

**TITLE** Direct Submission

**JOURNAL** Submitted (14-JAN-2000) Stroedel M., T.A.Trautner, Max-Planck-Institut fuer Molekulare Genetik, Ihnestrasse 73, 14195 Berlin, GERMANY

**COMMENT** [WARNING] On Jan 21, 2001 this sequence was replaced by a newer version gi:[12329972](#).

**FEATURES** Location/Qualifiers

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Range: from  to   Reverse complemented strand Features:  SNP  CDD  
 MGC  HPRD

1: [AF177473](#). Reports *Homo sapiens* MTR1...[gi:6715116]

Links

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 Hominidae; Homo.  
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 AUTHORS Prawitt,D., Enklaar,T., Klemm,G., Gartner,B., Spangenberg,C.,  
 Winterpacht,A., Higgins,M., Pelletier,J. and Zabel,B.  
 TITLE Identification and characterization of MTR1, a novel gene with  
 homology to melastatin (MLSN1) and the trp gene family located in  
 the BWS-WT2 critical region on chromosome 11p15.5 and showing  
 allele-specific expression  
 JOURNAL Hum. Mol. Genet. 9 (2), 203-216 (2000)  
 PUBMED [10607831](#)  
 REFERENCE 2 (bases 1 to 3913)  
 AUTHORS Prawitt,D., Pelletier,J. and Zabel,B.U.  
 TITLE Direct Submission  
 JOURNAL Submitted (13-AUG-1999) Children's Hospital, University of Mainz,  
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 LLIAMFSYTFQVVQGNADMFWKFQRYNLIVEYHERPALAPPFILLSHLSLTLLRVFKK  
 EAEEHKREHLERDLPDLDQKVVTWETVQKENFLSKMEKRRDSEGEVLRKTAHRVDFI  
 AKYLGGLREQEKRICKLESQINYCSVLVSSVADVLAQGGGPRSSQHCGEGLVAA  
 RGGGLDGWEQPGAGQPPSDT"

## ORIGIN

1 gaggccacca tgcaggatgt ccaaggcccc cgtcccgaa gccccgggaa tgctgaagac  
 61 cggcgggagc tgggcttgc a caggggcagc gtcaacttg gagggctctgg gaagaagcga  
 121 ggcaagtttg tacgggtgcc gagcggagtg g ccccgctctg tgctctttga cctgctctt  
 181 gctgagtggc acctgccgc ccccaacctg gtgggttccc tgggggtga ggagcagcct  
 241 ttcgccatga agtcctggct gcgggatgtg ctgcgcagg ggctgggtgaa ggccggctcag  
 301 agcacaggag cctggatcct gaccagtgc cccgcgtgg gcctggccag gcatgtcggg  
 361 caggccgtgc ggcaccactc gctggccagc acgtccacca agtccgtgt gtttgcgtc  
 421 ggcatggcct cgctgggccc cgtcctgcac cggccatcc tggaggaggc ccaggaggat  
 481 tttcctgtcc actaccctga g gatgacggc ggcagccagg gcccctctg ttcactggac  
 541 agcaacctct cccacttcat cctgggtggag ccaggcccc cggggaaaggc gatgggctg  
 601 acggagctgc ggctgaggtt ggagaagcac atctcgagc agagggcggg ctacggggc  
 661 actggcagca tcgagatccc tgcctctgc ttgctggta atggtgcatttcaacaccc  
 721 gagaggatct ccaggggccgt ggagcaggct gcccgtggc t gatcctgtt aggctcgaaa  
 781 ggcatcgcgc atgtgcttgc tgccttagt aaccagcccc acctcctgtt gccaagggtg  
 841 gccgagaagc agtttaagga ga ágtcccc agcaaggcatt tctttggaa ggacatcgtg  
 901 cgctggacca agctgctgca gacatcacc tcacaccgc acctgctcac cgttatgac  
 961 ttcgagcagg agggctccg g gagctggc acggtcatcc tgaaggcgc ggtaaagcc  
 1021 tgcaagagcc acagccagga g ctcaggac tatctggat agctcaagct gcccgtggcc  
 1081 tgggaccgcg tggacatcgc caagagttagt atcttcaatg gggacgtggaa gtggaaagtcc  
 1141 tgtgacctgg aggaggtgat ggtggacgccc ctggcagca acaagccca gtttgcgc  
 1201 ctctttgtgg acaacggcgc agacgtggcc gacttcctga cgtatggcgc gtcgcaggag  
 1261 ctctaccgcg ccgtgtcagc caagagcctg ctcttcgacc tgctgcagcg gaagcaggag  
 1321 gaggccggc tgacgctggc cggccctggc acccagcagg cccgggagcc acccgggggg  
 1381 ccacccgcct tctccctgca cgaggcttcc cgcgtactca aggacttcct gcaggacgccc  
 1441 tgccgaggct tctaccaggc cggccggcca ggggaccgca ggagggcggaa gaagggcccc  
 1501 gccaagccgc ccacgggcca gaagtggctg ctggacctga accagaagag cgagaacccc  
 1561 tggcgggacc tgttccctgtt ggccgtgtc cagaaccgc acgagatggc cacctacttc  
 1621 tgggccatgg gccaggaagg t g tggcagcc gcaactggcc cctgc aaaaat cctcaaaagag  
 1681 atgtcgacc tggagacgga g gccgaggcg gcccggacca cgcgcgaggc gaaatacgag  
 1741 cggctggccc ttgaccttctt ctccgagtgc tacagcaaca gtgaggcccg cgccttcgc  
 1801 ctgctgggtgc gccgaaaccg ctgctggagc a a g a c c a c t g c c t g c a c c t g g c a c c g a g  
 1861 gctgacgcca aggcccttctt t g c c c a c g a c g c g c g t t c a g g c t t c a g c  
 1921 tgggggaca tggccgcagg c a c g c c c a t c t g c g g c t g c t g a g g c c t t c t g c  
 1981 gcccctgtct ataccaaccc catcacccatc a g t g a g g a a g c t c c c t g a g g a c  
 2041 gaggacctgc aggacctgga c a g c c t g g a c a c g g a a g a g c t c c c t g c a g  
 2101 agccgggtgg aggagctggt ggaggcgcgg aggctcagg gtgaccgagg cccacgtct  
 2161 gtcttctgc tcacacgctg g c g g a a a t t c t g g g c g c t c c t g a c t g t g  
 2221 aacgtggtca t g t a c t t c g c t t c c t g a c t g t g a c t g t g  
 2281 aggccccc cccaggccc ctcaggccc gaggtcaccc t c t a c t t c t g g t c t t a c g  
 2341 ctggtgctgg aggaatccg g c a g g g c t t c t c a c a g a c g a g g a c a c a c a  
 2401 a a g t t c a c a c t g t a t g t g g g g a c a a g t g t g a c a t g g t g g c  
 2461 ttcatcgtgg gtgtcacctg caggatgtg c c g t c g g c g t t g a g g c t g g c  
 2521 ctcgccatgg a c t t c a t g g t g t c a c g c t g c g g c t g a t t c t t g c  
 2581 c a g c t g g g c c c a a g a t c a t c g g t a g a g c a t g a g g a c g t t  
 2641 t t c t t t c t g a g c t g g c t a c g t g t c a c c a c c g c g c t g c  
 2701 c a t g a c g g c c g c t g g a t t g a g a g c c c t a c t g c a g a t c  
 2761 t t c g g c c a g a g c t c a c t g g a c a g a t t g a g a g c c t a c  
 2821 c t g c t g c t g g a g g a c t c a c c a t c t g a c a c t g g c t g c  
 2821 c t g c t g c t g g a g g a c t c a c c a t c t g a c a c t g g c t g c

2881 ctgctggtca ctttcctgtt ggtcaccaat gtgctgtca tgaacctgtc catggccatg  
2941 ttcagctaca cgttccaggt ggtgcagggc aacgcagaca tttctggaa gttccagcgc  
3001 tacaacctga ttgtggagta ccacgagcgc cccgcctgg cccgcctt catctgtctc  
3061 agccacctga gcctgacgtc cgcgggtc ttcaagaagg aggtgagca caagcggag  
3121 cacctggaga gagacctgcc agaccccctg gaccagaagg tcgtcacctg ggagacagtc  
3181 cagaaggaga acttccttag caagatggag aagcggagga gggacagcga gggggaggtg  
3241 ctgcggaaaa ccccccacag agtggacttc attgccaagt acctcgaaaa gctgagagag  
3301 caagaaaagc gcatcaagtg tctggagtca cagatcaact actgctcggt gctcgtgtcc  
3361 tccgtggctg acgtgctggc ccagggtggc ggccccccgg a gctctcagca ctgtggcgag  
3421 ggaagccagc tgggtggctgc tgaccacaga ggtggtttag atggctggaa acaaccggg  
3481 gctggccagc ctccctcgga cacatgagct gcttggcctg ccacgtgtgg ggccacctct  
3541 cttagttgg ccaccctgca cgttgtgcac tgacctttgc cgacccctcag cggaaaccccc  
3601 cagggggcac cagccccca gcagacaatg gccctcctgg tgcctcacca cagaccctca  
3661 cccaaaggaa ccgcctccttg tccctcctgg cctccccgg a ggcacagcag tgcacatgggg  
3721 ctgtctcccc tgacaggcac aactccccgg gcagaaaacg tgcccccacccg catccctacc  
3781 tggaaactga ccagcctgca ctgtggaaaa gctggccctg tggcgtgacg ggggagcacc  
3841 cccatccaga ctgcgaagct gctctgggtc tgcacccacc cctgcccctga cttgtgttgc  
3901 ctgacaagag act

//

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Feb 9 2005 14:31:10

# Align two sequences

Tue Mar 1 21:52:38 "GMT 2005

```
/usr/tmp/seq1.73316.sca : 1158 aa
>Mouse MTR1, 1158 bases, 31D4F27D checksum. 1158 aa vs.
>Human MTR1, 1165 bases, C1D16397 checksum. 1165 aa
scoring matrix: , gap penalties: -12/-2
84.1% identity; Global alignment score: 6543
```

	10	20	30	40	50	60
/usr/t	MQTTQSSCPGSPPDTEDGWEPILCRGEINF	GGSGKKRGKFVKV	PSSVAPS	VLFELLTEW		
	::: ..	::::: ::::	::: :	::::: ::::	::::: ::::	::::: ::::
Human	MDVQGPRPGSPGDAEDRRELGLHRGEV	NFGSGKKRGKFVR	VPSGVAPS	VLFDL	LLAEW	
	10	20	30	40	50	60

	70	80	90	100	110	120
/usr/t	HLPAPNLVVSLVGEERPLAMKSWLRDVL	RKG	LVKAAQ	STGA	WILTSAL	HVG
	::::: ::::	::::: ::::	::::: ::::	::::: ::::	::::: ::::	::::: ::::
Human	HLPAPNLVVSLVGEEQPFAMKSWLRDVL	RKG	LVKAAQ	STGA	WILTSAL	RVG
	70	80	90	100	110	120

	130	140	150	160	170	180
/usr/t	RDHSLASTSTKIRVVAIGMASLDRILHRQL	LDGVH	QKEDTP	IHYPADEG	NIQGPLCPLDS	
	::::: ::::	::::: ::::	::::: ::::	::::: ::::	::::: ::::	::::: ::::
Human	RDHSLASTSTKVRVVAVGMASLGRVLHRR	ILE--	EAQEDFPV	HYPEDDGG	SQGPLCSLDS	
	130	140	150	160	170	

	190	200	210	220	230	240
/usr/t	NLSHFILVESGALGSGNDGLTELQLS	LEKHISQ	QRTGYGGT	SCIQIPV	LCLLVNGDP	NTL
	::::: ::	::::: ::	::::: ::	::::: ::	::::: ::	::::: ::
Human	NLSHFILVEPGPPKG-DGLTELRLR	LEKHIS	EQRAGYGGT	GSIIEIPV	LCLLVNGDP	NTL
	180	190	200	210	220	230

	250	260	270	280	290	300
/usr/t	ERISRAVEQAAPWLILAGSGGI	ADVLA	ALVSQPHLL	VPQVAE	KQFREKFP	SECFSWEAIV
	::::: ::::	::::: ::::	::::: ::::	::::: ::::	::::: ::::	::::: ::::
Human	ERISRAVEQAAPWLILVGSGGI	ADVLA	ALVNQPHLL	VPKVAE	KQFKEKFP	SKHFSWEDIV
	240	250	260	270	280	290

	310	320	330	340	350	360
/usr/t	HWTELLQNIAAHPLLTVYDFEQEGSE	DLDTVIL	KALVKACK	SHSQEAQD	YLDDEL	KLAVA
	::::: ::::	::::: ::::	::::: ::::	::::: ::::	::::: ::::	::::: ::::
Human	RWTKLLQNTSHQLLTVYDFEQEGSE	ELDTVIL	KALVKACK	SHSQEPQD	YLDDEL	KLAVA
	300	310	320	330	340	350

	370	380	390	400	410	420
/usr/t	WDRVDIAKSEIFNGDV	EWKSCD	LEEVMT	DALVSNK	PDFVRLF	VDSGADMAEFLTY
	::::: ::::	::::: ::::	::::: ::::	::::: ::::	::::: ::::	::::: ::::
Human	WDRVDIAKSEIFNGDV	EWKSCD	LEEV	MVDALVSNK	PEFVRLF	VDSGADMAEFLTY
	360	370	380	390	400	410

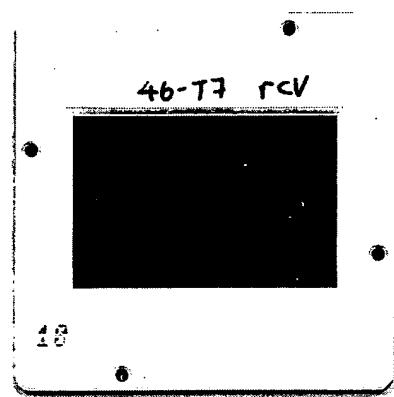
	430	440	450	460	470	480
/usr/t	LYHSVSPKSLLFELL	QRKHEEG	RLTLAGLGA	QQARELPI	GLPAFSL	HEVSRVLKDFLHDA
	::::: ::::	::::: ::::	::::: ::::	::::: ::::	::::: ::::	::::: ::::
Human	LYRSVSRKSLLFDLL	QRKQEE	EARLTLAGLGT	QQAREPPAG	PPAFSL	HEVSRVLKDFLQDA
	420	430	440	450	460	470

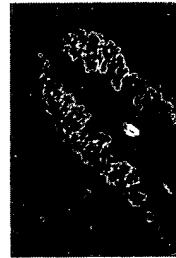
	490	500	510	520	530																																									
/usr/t	CRGFYQDGR	---RMEERGPPKRPAGQKWL	PDL	SRKSEDPW	RDLFLWAVL	QNRYEMATYF																																								
Human	CRGFYQDGR	PGD	RRAEK	GPAKRPTGQ	KWL	LDLNQKSEN	PW	RDLFLWAVL	QNRYEMATYF																																					
	480	490	500	510	520	530																																								
	540	550	560	570	580	590																																								
/usr/t	WAMGREGVAA	ALAACKII	KEMSH	LEKEA	EVART	MREAKY	EQLAL	DLFSECYGN	SEDR	AF																																				
Human	WAMQEGVAA	ALAACKI	KL	KEMSH	LETEA	AAARAT	MREAKY	ERLAL	DLFSECYS	NSEAR	AF																																			
	540	550	560	570	580	590																																								
	600	610	620	630	640	650																																								
/usr/t	LLVRRNHS	WSRTT	CLH	LATEAD	AKAFFA	HDGVQ	AFLTKI	WWGD	MATG	TPI	LRLG	AFTCP																																		
Human	LLVRRNRC	WSKTT	CLH	LATEAD	AKAFFA	HDGVQ	AFLTRI	WWGD	MAAG	TPI	LRLG	AFLCP																																		
	600	610	620	630	640	650																																								
	660	670	680	690	700	710																																								
/usr/t	ALIYTNLIS	FSEDAP	QRM	DLEDL	QEPDS	LDMEK	SFLCS	RGG	QLEK	LTEA	PRA	PAGD	LG	PQA																																
Human	ALVYTNLIT	TFSEE	PLRTG	LEDL	QDLD	SLDTEK	SPLYGL	QSR	VEEL	VEAP	RQA	GDRG	PRA																																	
	660	670	680	690	700	710																																								
	720	730	740	750	760	770																																								
/usr/t	AFLLTRW	RKF	WGAP	PTV	FLGN	VV	MYFA	FL	FTY	VLL	VD	FR	PPPQ	GP	SG	SE	VT	LY	FW	VFT																										
Human	VFLLTRW	RKF	WGAP	PTV	FLGN	VV	MYFA	FL	FTY	VLL	VD	FR	PPPQ	GP	SG	PE	VT	LY	FW	VFT																										
	720	730	740	750	760	770																																								
	780	790	800	810	820	830																																								
/usr/t	LVLEEIRQ	GFFT	DED	THLV	VKK	FTLY	VED	DNW	NKCD	MAI	FLF	I	VG	VT	CRM	VPS	V	FEA	GR	TV																										
Human	LVLEEIRQ	GFFT	DED	THLV	VKK	FTLY	VGD	DNW	NKCD	MAI	FLF	I	VG	VT	CRM	LPS	SAFE	GR	TV																											
	780	790	800	810	820	830																																								
	840	850	860	870	880	890																																								
/usr/t	LAIDFMV	FTLRLI	HIFAI	HKQLGP	KII	I	VERMM	KD	VFFF	FL	FL	SV	WL	VAY	GV	TT	Q	ALL	HP																											
Human	LAIDFMV	FTLRLI	HIFAI	HKQLGP	KII	I	VERMM	KD	VFFF	FL	FL	SV	WL	VAY	GV	TT	Q	ALL	HP																											
	840	850	860	870	880	890																																								
	900	910	920	930	940	950																																								
/usr/t	HDGRLEW	IFRRV	LYRP	YLQIFG	QIPL	DEI	DEAR	VNC	SLH	P	L	LE	S	ASCP	NLY	ANW	L	VIL																												
Human	HDGRLEW	IFRRV	LYRP	YLQIFG	QIPL	DEI	DEAR	VNC	STH	P	L	LE	SP	CP	SLY	ANW	L	VIL																												
	900	910	920	930	940	950																																								
	960	970	980	990	1000	1010																																								
/usr/t	LLVT	FLL	V	NV	V	L	M	N	L	I	A	M	F	W	K	F	Q	R	Y	H	G	R	P	A	L	A	P	P	F																	
Human	LLVT	FLL	V	NV	V	L	M	N	L	I	A	M	F	W	K	F	Q	R	Y	H	G	R	P	A	L	A	P	P	F																	
	960	970	980	990	1000	1010																																								
	1020	1030	1040	1050	1060	1070																																								
/usr/t	SHLS	LVL	KQV	F	R	K	E	A	Q	H	K	R	H	L	E	D	L	P	D	P	L	D	Q	V	V	T	W	E	T	V	Q	K	N	F												
Human	SHLS	LTL	RRV	F	K	E	A	H	K	R	H	L	E	D	L	P	D	P	L	D	Q	V	V	T	W	E	T	V	Q	K	N	F														
	1020	1030	1040	1050	1060	1070																																								
	1080	1090	1100	1110	1120	1130																																								
/usr/t	LRKTA	H	RV	D	L	I	A	K	Y	I	G	G	L	R	E	K	R	I	K	C	L	E	Q	A	N	C	M	L	L	S	S	M	T	D	L	A	P	G	G	T	Y	S	S	Q	N	C

## Sequence Alignment Output

Human	LRKTAHRVDFIAKYLGGLREQEKRIKCLSEQINYCSVLVSSVADVLAQGGGPRSSQHCGE
	1080 1090 1100 1110 1120 1130
	1140 1150
/usr/t	RSQPASARDREYLE-----SGLPPSDT
	: : . : . . . : : : :
Human	GSQLVAADHRGGLDGWEQPGAGQPPSDT
	1140 1150 1160

Elapsed time: 0:00:00





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